



RECEIVED

AUG 06 2002

TECH CENTER 1600/2900

78104023.ST25.txt

SEQUENCE LISTING

SAB
C1
<110> Gabriel, Panayi S
Corrigall, Valerie
Bodman-Smith, Mark
Fife, Mark
Danchbury, Jeremy

<120> Treatment of Inflammatory Disease

<130> 78104.023/N10984

<140> 09/806,955

<141> 2001-07-11

<150> PCT/GB99/03316

<151> 1999-10-08

<150> 9822115.3

<151> 1999-10-09

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 639

<212> PRT

<213> Homo sapiens

<400> 1

Met Glu Glu Asp Lys Lys Glu Asp Val Gly Thr Val Val Gly Ile Asp
1 5 10 15

Leu Gly Thr Thr Tyr Ser Cys Val Gly Val Phe Lys Asn Gly Arg Val
20 25 30

Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser Tyr Val
35 40 45

Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
50 55 60

78104023.ST25.txt

Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
65 70 75 80

Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
85 90 95

Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
100 105 110

Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
115 120 125

Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
130 135 140

Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
145 150 155 160

Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn
165 170 175

Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly
180 185 190

Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
195 200 205

Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe
210 215 220

Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
225 230 235 240

Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
245 250 255

78104023.ST25.txt

Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
260 265 270

Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
275 280 285

Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu
290 295 300

Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
305 310 315 320

Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
325 330 335

Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
340 345 350

Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro Ser Arg
355 360 365

Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
370 375 380

Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
385 390 395 400

Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
405 410 415

Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
420 425 430

Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys Val Tyr
435 440 445

78104023.ST25.txt

Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly Thr Phe
 450 455 460

Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu
 465 470 475 480

Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr Ala Glu
 485 490 495

Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
 500 505 510

Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
 515 520 525

Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
 530 535 540

Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp
 545 550 555 560

Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu Thr Met
 565 570 575

Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His Gln Asp
 580 585 590

Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu Glu Ile
 595 600 605

Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro Pro Pro
 610 615 620

Thr Gly Glu Glu Asp Thr Ala Glu Leu His His His His His His
 625 630 635

<210> 2
 <211> 633
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Glu Glu Asp Lys Lys Glu Asp Val Gly Thr Val Val Gly Ile Asp
 1 5 10 15

Leu Gly Thr Thr Tyr Ser Cys Val Gly Val Phe Lys Asn Gly Arg Val
 20 25 30

Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser Tyr Val
 35 40 45

Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
 50 55 60

Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
 65 70 75 80

Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
 85 90 95

Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
 100 105 110

Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
 115 120 125

Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
 130 135 140

Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
 145 150 155 160

Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn

165

170

175

Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly
 180 185 190

Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
 195 200 205

Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe
 210 215 220

Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
 225 230 235 240

Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
 245 250 255

Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
 260 265 270

Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
 275 280 285

Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu
 290 295 300

Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
 305 310 315 320

Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
 325 330 335

Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
 340 345 350

Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro Ser Arg

355

360

365

Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
 370 375 380

Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
 385 390 395 400

Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
 405 410 415

Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
 420 425 430

Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys Val Tyr
 435 440 445

Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly Thr Phe
 450 455 460

Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu
 465 470 475 480

Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr Ala Glu
 485 490 495

Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
 500 505 510

Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
 515 520 525

Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
 530 535 540

Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp

aaccgctgag 420

gcttatttgg gaaagaaggt tacccatgca gttgttactg taccagccta
ttttaatgat 480

gccaacgcc aagcaaccaa agacgctgga actattgctg gcctaaatgt
tatgaggatc 540

atcaacgagc ctacggcagc tgctattgct tatggcctgg ataagaggga
gggggagaag 600

aacatcctgg tgtttgacct ggggtggcgga accttcgatg tgtctcttct
caccattgac 660

aatgggtgtct tcgaagttgt ggccactaat ggagatactc atctgggtgg
agaagacttt 720

gaccagcgtg tcatggaaca cttcatcaaa ctgtacaaaa agaagacggg
caaagatgac 780

aggaaagaca atagagctgt gcagaaactc cggcgcgagg tagaaaaggc
caaacgggcc 840

ctgtcttctc agcatcaagc aagaattgaa attgagtcct tctatgaagg
agaagacttt 900

tctgagaccc tgactcgggc caaatttgaa gagctcaaca tggatctggt
ccggtctact 960

atgaagcccc tccagaaagt gttggaagat tctgatttga agaagtctga
tattgatgaa 1020

attgttcttg ttgggtggctc gactcgaatt ccaaagattc agcaactggg
taaagagtgc 1080

ttcaatggca aggaaccatc ccgtggcata aaccagatg aagctgtagc
gtatgggtgct 1140

gctgtccagg ctgggtgtgct ctctgggtgat caagatacag gtgacctggt
actgcttgat 1200

gtatgtcccc ttacacttgg tattgaaact gtgggagggtg tcatgaccaa
actgattcca 1260

aggaacacag tgggtgcctac caagaagtct cagatctttt ctacagcttc
tgataatcaa 1320

ccaactgtta caatcaaggt ctatgaaggt gaaagacccc tgacaaaaga

caatcatctt 1380

ctgggtacat ttgatctgac tggaattcct cctgctcctc gtgggggtccc
acagattgaa 1440

gtcacctttg agatagatgt gaatgggtatt cttcgagtga cagctgaaga
caagggtaca 1500

gggaacaaaa ataagatcac aatcaccaat gaccagaatc gcctgacacc
tgaagaaatc 1560

gaaaggatgg ttaatgatgc tgagaagttt gctgaggaag acaaaaagct
caaggagcgc 1620

attgatacta gaaatgagtt ggaaagctat gcctattctc taaagaatca
gattggagat 1680

aaagaaaagc tgggaggtaa actttcctct gaagataagg agaccatgga
aaaagctgta 1740

gaagaaaaga ttgaatggct ggaaagccac caagatgctg acattgaaga
cttcaaagct 1800

aagaagaagg aactggaaga aattgttcaa ccaattatca gcaaactcta
tggaagtga 1860

ggccctcccc caactggtga agaggatata gcagaactcc accaccacca ccaccac
1917

<210> 4
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 4
tatacatatg gaggaggaca agaaggagga cg
32

<210> 5
<211> 32
<212> DNA
<213> Artificial sequence

<220>

<223> Primer

<400> 5

ccacctcgag ttctgctgta tcctcttcac ca
32

<210> 6

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Isolated peptide fragment

<400> 6

Asn	Gln	Leu	Thr	Ser	Asn	Pro	Glu	Asn	Thr	Val	Phe	Asp	Ala	Lys
1				5					10					15

<210> 7

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> Isolated peptide fragment

<400> 7

Ser	Asp	Ile	Asp	Glu	Ile	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg
1				5					10				

<210> 8

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Isolated peptide fragment

<400> 8

Thr	Trp	Asn	Asp	Pro	Ser	Val	Gln	Gln	Asp	Ile	Lys
1				5					10		

<210> 9
 <211> 2554
 <212> DNA
 <213> Homo sapiens

<400> 9
 aggtcgacgc cggccaagac agcacagaca gattgaccta ttgggggtgtt
 tcgcgagtgt 60

gagaggggaag cgccgcggcc tgtatttcta gacctgccct tcgcctgggtt
 cgtggcgcct 120

tgtgaccccg gggccctgcc gcctgcaagt cggaaattgc gctgtgctcc
 tgtgctacgg 180

cctgtggctg gactgcctgc tgctgcccaa ctggctggca agatgaagct
 ctccctggtg 240

gcccgcgatgc tgctgctgct cagcgcggcg cgggccgagg aggaggacaa
 gaaggaggac 300

gtgggcacgg tggtcggcat cgacttgggg accacctact cctgcgtcgg
 cgtgttcaag 360

aacggcccg tggagatcat cgccaacgat cagggaacc gcatcacgcc
 gtcctatgtc 420

gccttcactc ctgaagggga acgtctgatt ggcgatgccg ccaagaacca
 gtcacctcc 480

aaccccgaga acacggtcct tgacgccaa cggctcatcg gccgcacgtg
 gaatgaccg 540

tctgtgcagc aggacatcaa gttcttgccg ttcaagggtg ttgaaaagaa
 aactaaacca 600

tacattcaag ttgatattgg aggtgggcaa acaaagacat ttgctcctga
 agaaatttct 660

gccatggttc tcactaaaat gaaagaaacc gctgaggctt atttgggaaa
 gaaggttacc 720

catgcagttg ttactgtacc agcctatctt aatgatgcc aacgccaagc
 aaccaagac 780

gctggaacta ttgctggcct aaatgttatg aggatcatca acgagcctac

ggcagctgct 840

attgcttatg gcctggataa gagggagggg gagaagaaca tcctgggtgtt
tgacctgggt 900ggcggaacct tcgatgtgtc tcttctcacc attgacaatg gtgtcttcga
agttgtggcc 960actaatggag atactcatct ggggtggagaa gactttgacc agcgtgtcat
ggaacacttc 1020atcaaactgt acaaaaagaa gacgggcaaa gatgtcagga aggacaatag
agctgtgcag 1080aaactccggc gcgaggtaga aaaggccaag gccctgtctt ctcagcatca
agcaagaatt 1140gaaattgagt ccttctatga aggagaagac ttttctgaga ccctgactcg
ggccaaattt 1200gaagagctca acatggatct gttccggtct actatgaagc ccgtccagaa
agtgttgaa 1260gattctgatt tgaagaagtc tgatattgat gaaattgttc ttgttggtgg
ctcgactcga 1320attccaaaga ttccagcaact ggttaaagag ttcttcaatg gcaaggaacc
atcccgtggc 1380ataaaccag atgaagctgt agcgtatggt gctgctgtcc aggctgggtgt
gctctctggt 1440gatcaagata caggtgacct ggtactgctt catgtatgtc cccttacact
tggtattgaa 1500actgtaggag gtgtcatgac caaactgatt ccaagtaata cagtgggtgcc
taccaagaac 1560tctcagatct tttctacagc ttctgataat caaccaactg ttacaatcaa
ggtctatgaa 1620ggtgaaagac ccctgacaaa agacaatcat cttctgggta catttgatct
gactggaatt 1680cctcctgctc ctggtggggg cccacagatt gaagtcacct ttgagataga
tgtgaatggt 1740

attcttcgag tgacagctga agacaagggt acagggaaca aaaataagat

78104023.ST25.txt

cacaatcacc 1800

aatgaccaga atcgccctgac acctgaagaa atcgaaagga tggttaatga
tgctgagaag 1860

tttgctgagg aagacaaaaa gctcaaggag cgcattgata ctagaaatga
gttggaagc 1920

tatgcctatt ctctaaagaa tcagattgga gataaagaaa agctgggagg
taaactttcc 1980

tctgaagata aggagaccat ggaaaaagct gtagaagaaa agattgaatg
gctggaaagc 2040

caccaagatg ctgacattga agacttcaaa gctaagaaga aggaactgga
agaaattgtt 2100

caaccaatta tcagcaaact ctatggaagt gcaggccctc cccaactgg
tgaagaggat 2160

acagcagaaa aagatgagtt gtagacactg atctgctagt gctgtaatg
tgtaaatact 2220

ggactcagga acttttgtta ggaaaaaatt gaaagaactt aagtctcgaa
tgtaattgga 2280

atcttcacct cagagtggag ttgaactgct atagcctaag cggctgttta
ctgcttttca 2340

ttagcagttg ctcacatgtc tttgggtggg gggggagaag aagaattggc
catcttaaaa 2400

agcgggtaaa aaacctgggt taggggtgtgt gttcaccttc aaaatgttct
atttaacaac 2460

tgggtcatgt gcatctgggt taggaagttt tttctaccat aagtgcacc
aataaatgtt 2520

tgttattttac actgggtcaaa aaaaaaaaaa aaaa
2554